

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 28, 2003, 13:49:30 ; Search time 26 Seconds
(without alignments)
3412.772 Million cell updates/sec

Title: US-09-497-822C-19
Perfect score: 4912
Sequence: 1 MEVQLGLGRVYRPPSKTYR.....SVQVPKILSGKVRPIVFIHQ 923
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4880	99.3	919	2 A39248	androgen receptor
2	4798.5	97.7	910	2 A34721	androgen receptor
3	4763	97.0	911	2 B34721	androgen receptor
4	4206.5	85.6	902	2 B40494	androgen receptor
5	4176	85.0	899	2 A35895	androgen receptor
6	1676	34.1	344	2 I51330	androgen receptor
7	1523	31.0	848	2 JG0194	androgen receptor
8	1262.5	25.7	930	2 A25923	androgen receptor
9	1262	25.7	933	1 ORHUP	progesterone recep
10	1234	25.1	923	2 I53280	progesterone recep
11	1218	24.8	786	2 A35466	progesterone recep
12	1205	24.5	923	2 A39596	progesterone recep
13	1092	22.2	981	2 A41401	progesterone recep
14	1078.5	22.0	984	2 A29513	mineralocorticoid
15	1065	21.7	795	1 ORSTG	mineralocorticoid
16	1063.5	21.7	783	1 A25691	glucocorticoid rec
17	1054.5	21.5	776	1 A44047	glucocorticoid rec
18	1042	21.2	777	1 ORHUGA	glucocorticoid rec
19	1023	20.8	758	2 S60586	glucocorticoid rec
20	1003	20.4	771	2 A54273	glucocorticoid rec
21	943.5	19.2	742	1 ORHUGB	glucocorticoid rec
22	715	14.6	166	2 S35795	glucocorticoid rec
23	502	10.2	595	2 I47140	androgen receptor
24	491	10.0	586	1 ORXLE	estradiol receptor
25	485.5	9.9	600	1 ORRTE	estrogen receptor
26	478	9.7	595	1 ORHUE	estrogen receptor
27	478	9.7	701	2 S64737	estrogen receptor
28	474	9.6	589	1 ORCHE	80K estrogen recep
29	474	9.6	599	1 ORNSE	estrogen receptor

30	461.5	9.4	620	2 T10423	estrogen receptor
31	448	9.1	535	2 S58224	estrogen receptor
32	444	9.0	574	2 A37197	estrogen receptor
33	442	9.0	503	2 JW0046	estrogen receptor
34	437.5	8.9	477	2 S71400	estrogen receptor
35	437.5	8.9	530	2 JC5939	estrogen receptor
36	398.5	8.1	1043	2 T13733	estrogen receptor
37	391	8.0	433	2 S58087	estrogen receptor
38	387.5	7.9	433	2 B29345	estrogen receptor
39	383	7.8	521	2 A29345	estrogen receptor
40	379	7.7	462	2 S44490	estrogen receptor
41	370.5	7.5	543	2 A32693	estrogen receptor
42	364.5	7.4	746	2 B32693	estrogen receptor
43	357	7.3	533	2 S37781	estrogen receptor
44	346	7.0	422	2 I48305	estrogen receptor
45	343.5	7.0	423	2 S02710	estrogen receptor

ALIGNMENTS

RESULT 1
A39248
androgen receptor - human
C:Species: Homo sapiens (man)
C:Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 24-Nov-1999
C:Accession: A39248; A39248; A40109; A60946; A34942; A27653; A40108; A40494; A32224;
R:Lubahn, D.B.; Brown, T.R.; Simental, J.A.; Higgins, H.N.; Migeon, C.J.; Wilson, E.M.;
Proc. Natl. Acad. Sci. U.S.A. 86, 9534-9538, 1989
A:Title: Sequence of the intron/exon junctions of the coding region of the human andr
A:Reference number: A39248; MUID:90083302; PMID:2594783
A:Accession: A39248
A:Molecule type: DNA
A:Residues: 1-919 <LU0>
A:Cross-references: GB:M27423; GB:M27430; NID:g178904; PIDN:AAA51886.1; PID:g178906
R:Faber, P.W.; Kuiper, G.G.J.M.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Brinkma
Mol. Cell. Endocrinol. 61, 257-262, 1989
A:Title: The N-terminal domain of the human androgen receptor is encoded by one, larg
A:Reference number: A30328; MUID:89137730; PMID:2917688
A:Accession: A30328
A:Molecule type: DNA
A:Residues: 1-77,779-165, 'A', 167-389, 'L', 391-464, 473-538 <FAB>
A:Cross-references: GB:M20260
R:Lubahn, D.B.; Joseph, D.R.; Sullivan, P.M.; Willard, H.F.; French, F.S.; Wilson, E.
Science 240, 327-330, 1988
A:Title: Cloning of human androgen receptor complementary DNA and localization to the
A:Reference number: A40109; MUID:88178112; PMID:3353727
A:Accession: A40109
A:Molecule type: DNA
A:Residues: 559-624 <LU2>
A:Cross-references: GB:M20132
R:Kuiper, G.G.J.M.; Faber, P.W.; van Rooij, H.C.J.; van der Korput, J.A.G.M.; Ris-Sta
J. Mol. Endocrinol. 2, R1-R4, 1989
A:Title: Structural organization of the human androgen receptor gene.
A:Reference number: A60946; MUID:89322749; PMID:2546571
A:Accession: A60946
A:Molecule type: DNA
A:Residues: 536-540; 587-591; 626-631; 723-726; 770-774; 814-818; 867-870 <KUI>
R:Lubahn, D.B.; Joseph, D.R.; Sar, M.; Tan, J.; Higgins, H.N.; Larson, R.E.; French, F.
Mol. Endocrinol. 2, 1265-1275, 1988
A:Title: The human androgen receptor: complementary deoxyribonucleic acid cloning, se
A:Reference number: A34942; MUID:89112208; PMID:3216866
A:Accession: A34942
A:Molecule type: mRNA
A:Residues: 1-919 <LU3>
A:Cross-references: GB:M20132; NID:g178627; PIDN:AAA51729.1; PID:g178628; GB:J03180
R:Trapan, J.; Klaassen, P.; Kuiper, G.G.J.M.; van der Korput, J.A.G.M.; Faber, P.W.;
Biochem. Biophys. Res. Commun. 153, 241-248, 1988
A:Title: Cloning, structure and expression of a cDNA encoding the human androgen rece
A:Reference number: A27653; MUID:88240407; PMID:3377788
A:Accession: A27653
A:Molecule type: mRNA
A:Residues: 468-564, 'K', 566-919 <TRA>

[illegible]

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A>Title: Specific region
A:Reference number: A34
A:Accession: A34721
A:Molecule type: mRNA
A:Residues: 1-910 <GOV>
C:Superfamily: unassigned
C:Keywords: zinc finger
F:548-806/Domain: erba
F:550-570/Region: zinc
F:586-610/Region: zinc
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QY	1	MEVQLGLGRVYPRPPSKTYGAFONLQFSQVREVIONPGPHPEAASAAAPGASLLLOQO	6
Db	1	MEVQLGLGRVYPRPPSKTYGAFONLQFSQVREVIONPGPHPEAASAAAPGASLLLL---	57
QY	61	QQQQQQQQQQQQQQQQQQQQQQQQQQQQETSPRQQQQQQQGGGSPQAHRGGTGYLVLDEEQPQS	12
	58	---QQQQQQQQQQQQQQQQQQQQETSPRQQQQQQGGGSPQAHRGGTGYLVLDEEQPQS	11

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QY 121 POSALECHPERGCVPEPAAVAASKGLPQQLPAPPPDEDDSAAPSTLSLLGTPFGLSSCS 180
Db 116 POSALECHPERGCVPEPAAVAASKGLPQQLPAPPPDEDDSAAPSTLSLLGTPFGLSSCS 175
QY 181 ADLKILSEASTMQLLQOOQOQFAYSEGSSSGRAREASGAPTSSKNDYLGSTSTISDNAKE 240
Db 176 ADLKILSEASTMQLLQOOQOQFAYSEGSSSGRAREASGAPTSSKNDYLGSTSTISDNAKE 235
QY 241 LCKAVSVSMGLGVEALEHLSPEGLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDSDS 300
Db 236 LCKAVSVSMGLGVEALEHLSPEGLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDSDS 295
QY 301 AGKSTEDTAESYSPKGGYTKGLESGSGSAAAGSSGTLPELSTLSLYKSGALDEAAA 360
Db 296 AGKSTEDTAESYSPKGGYTKGLESGSGSAAAGSSGTLPELSTLSLYKSGALDEAAA 355
QY 361 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAACRYGDLASLHGAG 420
Db 356 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAACRYGDLASLHGAG 415
QY 421 AAGPGSGSPSAASSSWHTLFTAEGLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480
Db 416 AAGPGSGSPSAASSSWHTLFTAEGLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGGGG 467
QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGWVSRVPPPTCVKSEMGPWMDSYSGPYGD 540
Db 468 VAPYGYTRPPQGLAGQESDFTAPDVWYPGWVSRVPPPTCVKSEMGPWMDSYSGPYGD 527
QY 541 MRLETARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGCKVFFKRAAEGKQKYLCA 600
Db 528 MRLETARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGCKVFFKRAAEGKQKYLCA 587
QY 601 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQEEGASSTTSPTTEET 660
Db 588 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQEEGASSTTSPTTEET 647
QY 661 QKLTSHIEGECQIFLNVLEAIEPVGVCAGHNNQPDFAALLSSNLSLGERQLVHV 720
Db 648 QKLTSHIEGECQIFLNVLEAIEPVGVCAGHNNQPDFAALLSSNLSLGERQLVHV 707
QY 721 KWAKALPGRNLHVDDQMAVIOYSWGLMVFAMGWRSTTNVNSRMLYFAPDLVFNERYMH 780
Db 708 KWAKALPGRNLHVDDQMAVIOYSWGLMVFAMGWRSTTNVNSRMLYFAPDLVFNERYMH 767
QY 781 KSRMYSQVVRMRLHSQEFGLQITPQEFCLMKALLFSIIPVDGLKNQKPFDELRMYIK 840
Db 768 KSRMYSQVVRMRLHSQEFGLQITPQEFCLMKALLFSIIPVDGLKNQKPFDELRMYIK 827
QY 841 ELDRITACKRNKPTSCSRFFYOLTLLDSDVQPIARELHQFTFDLLIKSHMVSVDFPEMMA 900
Db 828 ELDRITACKRNKPTSCSRFFYOLTLLDSDVQPIARELHQFTFDLLIKSHMVSVDFPEMMA 887
QY 901 EIISVQVPKILSGKVKPIYFHTQ 923
Db 888 EIISVQVPKILSGKVKPIYFHTQ 910

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RESULT 3

B34721
 androgen receptor B - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 12-Sep-1997
 C:Accession: B34721
 R:Govindan, M.V.
 Mol. Endocrinol. 4, 417-427, 1990
 A:Title: Specific region in hormone binding domain is essential for hormone binding and
 A:Reference number: A34721; MUID:90258935; PMID:2342476
 A:Accession: B34721
 A:Molecule type: mRNA
 A:Residues: 1-911 <Go2>
 C:Superfamily: unassigned
 C:Keywords: zinc finger

F:548-806/Domain: erba transforming protein homology <ERBA>
 F:550-570/Region: zinc finger
 F:586-610/Region: zinc finger

Query Match 97.0%; Score 4763; DB 2; Length 911;
 Best Local Similarity 97.8%; Pred. No. 5,le-244;
 Matches 904; Conservative 1; Mismatches 5; Indels 14; Gaps 3;

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QY 1 MEVGLIGRIVPRPSPKTYRGAONLFQSVREVIONPGRPHPEAASAPPGASILLLOOQ 60
Db 1 MEVGLIGRIVPRPSPKTYRGAONLFQSVREVIONPGRPHPEAASAPPGASILLLOOQ 57
QY 61 QOOOQOOOQOOOQOOOQOOQOQETSPRQOOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 120
Db 58 --QOOOQOOOQOOOQOOOQOOQOQETSPRQOOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 115
QY 121 POSALECHPERGCVPEPAAVAASKGLPQQLPAPPPDEDDSAAPSTLSLLGTPFGLSSCS 180
Db 116 POSALECHPERGCVPEPAAVAASKGLPQQLPAPPPDEDDSAAPSTLSLLGTPFGLSSCS 175
QY 181 ADLKILSEASTMQLLQOOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 240
Db 176 ADLKILSEASTMQLLQOOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 235
QY 241 LCKAVSVSMGLGVEALEHLSPEGLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDSDS 300
Db 236 LCKAVSVSMGLGVEALEHLSPEGLRGDCMYAPLLGVPPAVRPTPCAPLAECGSLDSDS 295
QY 301 AGKSTEDTAESYSPKGGYTKGLESGSGSAAAGSSGTLPELSTLSLYKSGALDEAAA 360
Db 296 AGKSTEDTAESYSPKGGYTKGLESGSGSAAAGSSGTLPELSTLSLYKSGALDEAAA 355
QY 361 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAACRYGDLASLHGAG 420
Db 356 YQSRDYNFPLALAGPPPPPPHARIKLENPLDYGSAWAAAAACRYGDLASLHGAG 415
QY 421 AAGPGSGSPSAASSSWHTLFTAEGLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGGGG 480
Db 416 AAGPGSGSPSAASSSWHTLFTAEGLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGGGG 467
QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGWVSRVPPPTCVKSEMGPWMDSYSGPYGD 540
Db 468 VAPYGYTRPPQGLAGQESDFTAPDVWYPGWVSRVPPPTCVKSEMGPWMDSYSGPYGD 527
QY 541 MRLETARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGCKVFFKRAAEGKQKYLCA 600
Db 528 MRLETARDHVLPIIDYFPPOKTLICGDEASGCHYGALTCGCKVFFKRAAEGKQKYLCA 587
QY 601 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQEEGASSTTSPTTEET 660
Db 588 SRNDCTIDKFRKNCPSCLRKCYEAGMTLGARKLKLGNLKLQEEGASSTTSPTTEET 647
QY 661 QKLTSHIEGECQIFLNVLEAIEPVGVCAGHNNQPDFAALLSSNLSLGERQLVHV 720
Db 648 QKLTSHIEGECQIFLNVLEAIEPVGVCAGHNNQPDFAALLSSNLSLGERQLVHV 707
QY 721 KWAKALPGRNLHVDDQMAVIOYSWGLMVFAMGWRSTTNVNSRMLYFAPDLVFNERYMH 780
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QY 781 KSRMYSQVVRMRLHSQEFGLQITPQEFCLMKALLFSIIPVDGLKNQKPFDELRMYIK 840
Db 768 KSRMYSQVVRMRLHSQEFGLQITPQEFCLMKALLFSIIPVDGLKNQKPFDELRMYIK 827
QY 840 KELDRIITACKRNKPTSCSRFFYOLTLLDSDVQPIARELHQFTFDLLIKSHMVSVDFPEMMA 899
Db 828 KELDRIITACKRNKPTSCSRFFYOLTLLDSDVQPIARELHQFTFDLLIKSHMVSVDFPEMMA 887
QY 900 AEIISVQVPKILSGKVKPIYFHTQ 923
Db 888 AEIISVQVPKILSGKVKPIYFHTQ 911

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RESULT 4
B40494
androgen receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Sep-1999
C:Accession: B40494; A34943; A36283; B40108
R:Chang, C.; Kokontis, J.; Liao, S.
Proc. Natl. Acad. Sci. U.S.A. 85, 7211-7215, 1988
A:Title: Structural analysis of complementary DNA and amino acid sequences of human and
A:Reference number: A40494; MUID:89017168; PMID:3174628
A:Accession: B40494
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-902 <CHA>
A:Cross-references: GB:M23264; NID:g202967; PIDN:AAA40759.1; PID:g202968
R:Tan, J.; Joseph, D.R.; Quarumby, V.E.; Lubahn, D.B.; Sar, M.; French, F.S.; Wilson, E.M.
Mol. Endocrinol. 2, 1276-1285, 1988
A:Title: The rat androgen receptor: primary structure, autoregulation of its messenger
A:Reference number: A34943; MUID:89112209; PMID:3216867
A:Accession: A34943
A:Molecule type: mRNA
A:Residues: 1-388, 'S', 390-902 <TAN>
A:Cross-references: GB:M20133; NID:g202895; PIDN:AAA40733.1; PID:g202896
R:Yarabough, W.G.; Quarumby, V.E.; Simental, J.A.; Joseph, D.R.; Sar, M.; Lubahn, D.B.;
J. Biol. Chem. 265, 8893-8900, 1990
A:Title: A single base mutation in the androgen receptor gene causes androgen insensitivity
A:Reference number: A36283; MUID:90256822; PMID:2341409
A:Accession: A36283
A:Molecule type: mRNA
A:Residues: 1-194, 196-902 <VAR>
A:Cross-references: GB:J05454
R:Chang, C.; Kokontis, J.; Liao, S.
Science 240, 324-326, 1988
A:Title: Molecular cloning of human and rat complementary DNA encoding androgen receptor
A:Reference number: A40108; MUID:88178111; PMID:3353726
A:Accession: B40108
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 540-611 <CH2>
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; zinc finger
F:540-798/Domain: erba transforming protein homology <ERBA>
F:542-562/Region: zinc finger
F:578-602/Region: zinc finger

Query Match 85.6%; Score 4206.5; DB 2; Length 902;
Best Local Similarity 84.7%; Pred. No. 1.2e-214;
Matches 797; Conservative 36; Mismatches 51; Indels 57; Gaps 4;

QY 1 MEVQLGLGRVYPRPSTKTYRGAFQNLFSVREVTONPGRHPEAASAPPGASILLILQQQ 60
DB 1 MEVQLGLGRVYPRPSTKTYRGAFQNLFSVREVTONPGRHPEAASAPPGASILLILQQQ 60

QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
DB 55 -----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 96

QY 120 QPQSALECHPERGCVPEPAAVAASKGLPQQLPAPPDEDDSAAPSTSLIGPTFPGLSSC 179
DB 97 QQQSASEGHPESCGLEPQAATAPKGLPQQPPAPPDQDDSAAPSTSLIGPTFPGLSSC 156

QY 180 SADKIDLSASTMQLL-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 222
DB 157 SADKIDLSASTMQLL-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 216

QY 223 SKNYLGSTTISDNKELKAVSVSMGLGVEALEHLSPEGLRGDCMYPALLGVPPAVR 282
DB 217 SKDYLGNSTISDSKELKAVSVSMGLGVEALEHLSPEGLRGDCMYPALLGVPPAVR 276

QY 283 PTPCAPLAECKSLDDDSACKSTEDTAETSPFKGGYTKGLESGCSGSAAGSGTLE 342
DB 277 PTPCAPLAECKSLDEPGPKGTETAEYSFSGKYAKGLESGCSGSAAGSGTLE 336

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QY 403 AAAACRYGDLASLHGAGAGPGSGSPSAASSSSWHTLFTAEGLYPCGGGGGGGGG 462
DB 397 AAAACRYGDLASLHGAGAGPGSGSPSAASSSSWHTLFTAEGLYPCGGGGGGGGG 445
QY 463 GGGGGGGGGGGGGGAGAVPYGYTRPPQGLAGQSDFTAPDVWYPGWVSRVYPSP 522
DB 446 ----GGGGGGSSPSDAGVPYGYTRPPQGLASQSGDFSASEVWYPGWVSRVYPSP 501
QY 523 VKSEMPNMDSYSGPYGDMRLDSTRDHLPLIDYPPQKTCICGDEASGCHYALTCGS 582
DB 502 VKSEMPNMDSYSGPYGDMRLDSTRDHLPLIDYPPQKTCICGDEASGCHYALTCGS 561
QY 583 CKVFFRAEGKQKYLCAASNDCTDKFRKNCPCRLKRCYKYEAGMTLGARLKLGLN 642
DB 562 CKVFFRAEGKQKYLCAASNDCTDKFRKNCPCRLKRCYKYEAGMTLGARLKLGLN 621
QY 643 LQEGEASSTTSPTETTKLVSHIEGYECQIFLNVLAEIPEGVVCGAGHNNQPSFA 702
DB 622 LQEGEASSTTSPTETTKLVSHIEGYECQIFLNVLAEIPEGVVCGAGHNNQPSFA 681
QY 703 ALLSSNELGEROLVHVWKAALPGFRNLHYDDQNAVIOYSWMLGMVFMGWSFTNN 762
DB 682 ALLSSNELGEROLVHVWKAALPGFRNLHYDDQNAVIOYSWMLGMVFMGWSFTNN 741
QY 763 SRMLYFAPDLVFNEMHKSRYMYSQVVRHLSQEGWLIQITPQEFLLCMKALLSIPV 822
DB 742 SRMLYFAPDLVFNEMHKSRYMYSQVVRHLSQEGWLIQITPQEFLLCMKALLSIPV 801
QY 823 DGLKNQKFFDELNMNLIKELDRITIAKRNKPTSCSRFVQLTKLLDSVQPIARELH 882
DB 802 DGLKNQKFFDELNMNLIKELDRITIAKRNKPTSCSRFVQLTKLLDSVQPIARELH 861
QY 883 DLLIKSHMVSDVPEMMAEIIISVQVKILSGKVKPIYFHTQ 923
DB 862 DLLIKSHMVSDVPEMMAEIIISVQVKILSGKVKPIYFHTQ 902

RESULT 5
A35895
androgen receptor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Oct-1990 #sequence_revision 31-Oct-1990 #text_change 20-Sep-1999
C:Accession: A35895; A37255; A37908; S34398; S17198; S40626; I49501; S12082
R:He, W.W.; Fischer, L.M.; Sun, S.; Billhartz, D.L.; Zhu, X.; Young, C.Y.F.; Kelley, D.
Biochem. Biophys. Res. Commun. 171, 697-704, 1990
A:Title: Molecular cloning of androgen receptors from divergent species with a polym
A:Reference number: A35895; MUID:90386642; PMID:2403358
A:Accession: A35895
A:Molecule type: mRNA
A:Residues: 1-899 <HEA>
A:Cross-references: EMBL:X53779; NID:g49966; PIDN:CAA37795.1; PID:g49967
R:Gaspar, M.L.; Meo, T.; Tosi, M.
Mol. Endocrinol. 4, 1600-1610, 1990
A:Title: Structure and size distribution of the androgen receptor mRNA in wild-type a
A:Reference number: A37255; MUID:91133433; PMID:2178222
A:Accession: A37255
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-899 <GAS>
A:Cross-references: GB:M37890; NID:g191935; PIDN:AAA37234.1; PID:g191936
R:Charest, N.J.; Zhou, Z.; Lubahn, D.B.; Olsen, K.L.; Wilson, E.M.; French, F.S.
Mol. Endocrinol. 5, 573-581, 1991
A:Title: A frameshift mutation destabilizes androgen receptor messenger RNA in the Tf
A:Reference number: A37908; MUID:92017874; PMID:1681426
A:Accession: A37908
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-899 <CHA>

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A:Cross-references: GB:856385; NID:92336048; PIDN:AAB19916.1; PID:92336049
R:Faber, P.W.; King, A.; van Rooij, H.C.J.; Brinkmann, A.O.; de Both, N.J.; Trapman, J.
Blochem. J. 278, 269-278, 1991
A:Title: The mouse androgen receptor. Functional analysis of the protein and characterization of the androgen receptor gene.
A:Reference number: S17198; MUID:91354214; PMID:1883336
A:Accession: S34398
A:Molecule type: DNA
A:Residues: 1-899 <FAB>
A:Cross-references: EMBL:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
A:Accession: S17198
A:Molecule type: mRNA
A:Residues: 1-899 <FAB>
A:Cross-references: GB:X59592; NID:949968; PIDN:CAA42160.1; PID:949969
R:He, W.W.; Kumar, M.V.; Tindall, D.J.
Nucleic Acids Res. 19, 2373-2378, 1991
A:Title: A frame-shift mutation in the androgen receptor gene causes complete androgen insensitivity syndrome.
A:Reference number: S40626; MUID:91252278; PMID:2041777
A:Accession: S40626
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 366-413 <HEW>
A:Cross-references: EMBL:X53779
R:Gaspar, M.
Proc. Natl. Acad. Sci. U.S.A. 88, 8606-8610, 1991
A:Title: A single base deletion in the α androgen receptor gene creates a short-lived protein.
A:Reference number: I49501; MUID:92020902; PMID:1924321
A:Accession: I49501
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-899 <RES>
A:Cross-references: GB:M37890; NID:9191935; PIDN:AAA37234.1; PID:g191936
C:Genetics:
A:Introns: 518/2; 569/1; 608/1; 704/1; 752/2; 796/1; 848/3
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger
F:1-536/Domain: regulatory status predicted <REG>
F:537-795/Domain: regulatory status predicted <REG>
F:539-559/Region: erba transforming protein homology <ERBA>
F:575-599/Region: zinc finger
F:650-899/Domain: hormone binding #status predicted <LIG>

Query Match 85.0%; Score 4176; DB 2; Length 899;
Best Local Similarity 84.1%; Pred. No. 4.8e-213;
Matches 790; Conservative 40; Mismatches 53; Indels 56; Gaps 5;

QY 1 MEVQLGLGRVYPRPSKTYRGAFONLQSVREVIONPGPHRPAASAPPGASLLLLQQO 60
Db 1 MEVQLGLGRVYPRPSKTYRGAFONLQSVREVIONPGPHRPAASAPPGASLLLLQQO 60
QY 61 QQQ 119
Db 55 -----QQ 119
QY 120 QPQSALECHPRGCVPRPAAVAAKGLPQALPAPDEDDSAAPSTLSLLGPTFGLSSC 179
Db 120 QPQSALECHPRGCVPRPAAVAAKGLPQALPAPDEDDSAAPSTLSLLGPTFGLSSC 179
QY 97 QQQAASECHPSSCLPFGAATAPGKLPQPPAPPDQDDSAAPSTLSLLGPTFGLSSC 156
Db 97 QQQAASECHPSSCLPFGAATAPGKLPQPPAPPDQDDSAAPSTLSLLGPTFGLSSC 156
QY 180 SADLKDILSEASTMQLQ-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 224
Db 180 SADLKDILSEASTMQLQ-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 224
QY 157 SADIKDILNEAGTMQLQ-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 215
Db 157 SADIKDILNEAGTMQLQ-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 215
QY 225 DNYLGSTSTSDNAKELCAVSMGLGVEALEHLSLPGQLRDCDCMYAPLLGVPVAVRPT 284
Db 225 DNYLGSTSTSDNAKELCAVSMGLGVEALEHLSLPGQLRDCDCMYAPLLGVPVAVRPT 284
QY 216 DSYLGSTSTSDNAKELCAVSMGLGVEALEHLSLPGQLRDCDCMYAPLLGVPVAVRPT 275
Db 216 DSYLGSTSTSDNAKELCAVSMGLGVEALEHLSLPGQLRDCDCMYAPLLGVPVAVRPT 275
QY 285 PCAPLAECGSLDSDAGKSTEDTAETSPFKGTYKGLGESLGCSSGAAGSSGSLLEP 344
Db 285 PCAPLAECGSLDSDAGKSTEDTAETSPFKGTYKGLGESLGCSSGAAGSSGSLLEP 344
QY 276 PCAPLPECKGLPDEGPKSTETATYSSFKGYAKGLGESLGCSSGAAGSSGSLLEP 335
Db 276 PCAPLPECKGLPDEGPKSTETATYSSFKGYAKGLGESLGCSSGAAGSSGSLLEP 335
QY 345 STLSLYKSGALDAAAYQSRDYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWAA 404
Db 345 STLSLYKSGALDAAAYQSRDYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWAA 404
QY 336 SSLSLYKSGALDAAAYQSRDYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWAA 395
Db 336 SSLSLYKSGALDAAAYQSRDYNFPLALAGPPPPPPPPPPHARIKLENPLDYGSAWAA 395

QY 405 AAOCRYGLDASLHAGAGCGSPSAAASSSWHTLFTAEQGLYPCGCGGGGGGGGGG 464
Db 396 AAOCRYGLDASLHAGAGCGSPSAAASSSWHTLFTAEQGLYPCGCGGGGGGGGGG 464
QY 465 GGG 442
Db 443 --GG 524
QY 525 SEMCPWMDSYSGPYGDMRLTARDHVLPIIDYFFPPQKTLICGDEASGCHFGALTCG 584
Db 501 SEMCPWMDSYSGPYGDMRLTARDHVLPIIDYFFPPQKTLICGDEASGCHFGALTCG 584
QY 585 VFFKRAAEGKQKYLCAASRNDCTIDFRKNCPSCLRCYAGMTLGARKLKLGNLKLQ 644
Db 561 VFFKRAAEGKQKYLCAASRNDCTIDFRKNCPSCLRCYAGMTLGARKLKLGNLKLQ 620
QY 645 EGEASSTTSPTEETQKTLVSHIEGYEQPIFLNVLEAIEPFGVVCAGHNNQPDFAAL 704
Db 621 EGEASSTTSPTEETQKTLVSHIEGYEQPIFLNVLEAIEPFGVVCAGHNNQPDFAAL 680
QY 705 LSSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGLVFMAGHRSFTNNSR 764
Db 681 LSSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGLVFMAGHRSFTNNSR 740
QY 765 MLYFAPDLVFNRYMHKSRMYSCQVVRHLSQEFGLQITPOEFLCMKALLFSIIPVDG 824
Db 741 MLYFAPDLVFNRYMHKSRMYSCQVVRHLSQEFGLQITPOEFLCMKALLFSIIPVDG 800
QY 825 LKNQKFFDELRLNMIKELDRIIACKRNKPTSCSRFFVOLTLLKLDVSVQPIAKELHQFTFDL 884
Db 801 LKNQKFFDELRLNMIKELDRIIACKRNKPTSCSRFFVOLTLLKLDVSVQPIAKELHQFTFDL 860
QY 885 LKSHWVSDVPEMAEIIISVQVKILSGKVKPIYFHTQ 923
Db 861 LKSHWVSDVPEMAEIIISVQVKILSGKVKPIYFHTQ 899
RESULT 6
I51330
androgen receptor - common canary (fragment)
C:Species: Serinus canaria (common canary)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Sep-1999
C:Accession: I51330
R:Nastiuk, K.L.; Clayton, D.F.
Endocrinology 134, 640-649, 1994
A:Title: Seasonal and tissue-specific regulation of canary androgen receptor messenger RNA.
A:Reference number: I51330; MUID:94130808; PMID:8299561
A:Accession: I51330
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <NAS>
A:Cross-references: GB:L25901; NID:9414733; PIDN:AAAL7402.1; PID:9414734
C:Genetics:
A:Gene: AR
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: zinc finger
F:1-251/Domain: erba transforming protein homology (fragment) <ERBA>
Query Match 34.1%; Score 1676; DB 2; Length 344;
Best Local Similarity 30.4%; Pred. No. 1.5e-81;
Matches 311; Conservative 20; Mismatches 13; Indels -0; Gaps 0;
QY 569 EASGCHYALTCGCKVFFKRAAEGKQKYLCAASRNDCTIDFRKNCPSCLRCYAGM 628
Db 1 EASGCHYALTCGCKVFFKRAAEGKQKYLCAASRNDCTIDFRKNCPSCLRCYAGM 60
QY 629 TLGARKLKLGNLKLQEGEASSTTSPTEETQKTLVSHIEGYEQPIFLNVLEAIEPVG 688
Db 61 TLGARKLKLGNLKLQEGEASSTTSPTEETQKTLVSHIEGYEQPIFLNVLEAIEPVG 120
QY 689 VCAGHNNQPDFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGL 748
Db 121 VCAGHNNQPDFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDVDDMAVIOYSWMGL 180

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Db      387  FQYRNECSCTPSAPRHCAHQNRAGPYNQFFENPPEYAKRGVSVREGYSLGHEGPNNLA  446
QY      518  --PSPCTCVKSEMPWMDSYSGPYGDM--RLETARDHVLPIDYFFPQKTLICGDEASGC  573
Db      447  RTYPSGSLKNELG---DRUSGPPYDVSYRYEGRENVPVEFFFPQRTCLICGDEASGC  503
QY      574  HYGALTCGCKVFFKRAAEQKQYLCAASRNDCTIDKFRKNCPCSCRLRCYCEAGMTLGAR  633
Db      504  HYGALTCGCKVFFKRAAEQKQYLCAASINDCTIDKLRKNCPCSCRLKRCFAAGMTLGAR  563
QY      634  KLKLGKMLKLOEGEASSTPTTEOTKLTVS--HLEGVECOPIFLNVLEATEPGVVCA  691
Db      564  KLKIGOMRAPEDGGQ---GPAAE---AELUSPKYDGLGFHTSMFLNILEATEPEVNA  617
QY      692  GHDNNDPDSFAALLSNLSELGEROLVHVVKAKALPGFRNLHVDDQMAVTOYSGMGLMVF  751
Db      618  GHYDQPDASAASLLTSLNELGERLVKVKWAKGMPGFRSLYVDDQMTVQKHWMAVMVF  677
QY      752  AMGWRSTNNVNRMLYFAPDLVFNFYRMRHKSRYSCQVRMRHLSOEGWLQITPOEFLCM  811
Db      678  ALGWRSEFNKVRMLYFAPDLVFNHEHRMQVSTMEHCIRMKNFQSEFAMQLQVSOEFLCM  737
QY      812  KALLFSTIPVDGLKNOKFFDELBMNTIKELDRYIACKRNKNTSCSRFFQTLKLDVSQ  871
Db      738  KALLFSTIPVEGLKGQNFDELRRSYINELDRVLSFRSK--SSCSERFOQLTRLDSLQ  795
QY      872  PIARELHOFTFDLLIKSHWS--VDFPEMAEILISVOVPKILSGKVKPIYFH  921
Db      796  PVLKRLHOFTFDLFQVQSNLQNCQCFPEMISEILSVHVPKILAGTVRPILFH  847

RESULT 8
A25923
progesterone receptor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 20-Aug-1999
C:Accession: A25923
R:Loosfelt, H.; Atger, M.; Misrahi, M.; Guiochon-Mantel, A.; Meriel, C.; Logeat, F.;
Proc. Natl. Acad. Sci. U.S.A. 83, 9045-9049, 1986
A:Title: Cloning and sequence analysis of rabbit progesterone-receptor complementary
A:Reference number: A25923; MUID:87067449; PMID:3538016
A:Accession: A25923
A:Molecule type: mRNA
A:Residues: 1-930 <L00>
A:Cross-references: GB: M4547; MID: g15631; PIDN: AAA31443.1; PID: g15632
C:Superfamily: progesterone receptor; erba transforming protein.homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation
F:566-826/Domain: erba transforming protein homology <ERBA>
F:568-588/Region: zinc finger
F:604-628/Region: zinc finger

Query Match 25.7%; Score 1262.5; DB 2; Length 930;
Best Local Similarity 34.4%; Pred. No. 3e-59;
Matches 349; Conservative 127; Mismatches 313; Indels 225; Gaps 38;

QY      39  PRPEAASAPP-----GASILLILQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ-----  85
Db      9  PRAPHVAGGAPSTVEGSQL-----GRDPGPFQGSQTSEASSVVSAPITS  55
QY      86  -----PRQQQQQQGGEDGSPQ-----AHRRGP---TGVL--V  111
Db      56  LDGILLFPRPCQGGNPPDGKTDPPSLSDVEGAPFGVEAPEGAGDSSRRPERKDSGLDSV  115
QY      112  LDEEQQPSQ-----QSALECH-----PERGCVPEPGAAVAASKGLPQQLPAPPDE-  157
Db      116  LDTLLAPSGGQSHASPATCEAISPWCLFGPD---LPEDPRAAPATKGVLIAPLMSRPEDK  172
QY      158  --DDSA-----APSTLSLL---GpFPFGI-----SSCSADLKDLI-SEAST  192
Db      173  AGDSSGTAHAHKVLPRLGSLSPQLLLPSSGSPHPAVKPSQPQAAVOVDEEDSESEGTV  232
QY      193  MOLLQQQQQEEAVSEGGSSGAREASGAPTSKNYLGGTSTI-SDNAKELCAVSVSMGL  251

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Db 233 GPLLKQPRALGGTAAGGAAPVASGAAA-----GGVALVPKEDSRFSAPRVSLA---- 282
QY 252 GVEALEHLSPEQLRG-----DCMYAPLLGVPPAVRPTPCAPLAECKGSLDSDAGKST-- 305
Db 283 --EQDAPVAPGRSLATSVVDFIHPILPLNHAFLATRTQLLE--GESYDGGAAASPF 338
QY 306 -----EDTAESYSPKGG-----YTKLEGESIGCSGSAAGSGTLELPSTLSLYKSGA 354
Db 339 VPQGSFASSTPVAGGDFDCTYPPDAEPK-----DDAFPLYGDFQ--PPALKIKEE 391
QY 355 LDEAAAYQSRDY-----NFP--LALAGPPPPPPHARKLENPLDLYGSANAAAA 406
Db 392 AAEAAARSPTLYVAGANPAAPDFQLAAPPPSLPP-----RVPSSRP--GEA----- 438
QY 407 QCRVGLASLHAGAGAGPGSGPSAAASSWH---TLFTAE-----EGOLY-PCGGGG 457
Db 439 -----AAVASPGGSASVSSSSSGSTLECLYKAEGAPPOGFPAPLCKPPGA 486
QY 458 GGGGGGGGGGGGGGGGGGAGAVPYGYTRPPQGLAGSDFTPADPVWYGMVSR--- 514
Db 487 GACLLPRDGLPSTASGAAGAAPALY-----PTLGLNG-----LPOLGYQAAVLKEGLP 536
QY 515 ---VPSPCTVKSEMPMMDSYSGPYGDMRLTARDHVLPIDYFP--POKTLICGDE 569
Db 537 QVYTPY-----LNLYRPDSEASQSP-----QYSFESLPKICLICGDE 574
QY 570 ASGCHYGALTCGCKVFFKRAEGKOKYLACARNDCITDKFRKNCPSCLRLKCYEAGMT 629
Db 575 ASGCHGVLTCGCKVFFKRAEGQHNYLACGRNDCIYDKIRKNCACRLKCCQAGW 634
QY 630 LGARKLKLNKLKLOEGEASSTTPT--EETQKLTVSHTEGYECOPIFLNLEATEPG 687
Db 635 LGGRKFKTKVKNVRMALDAVALPOVGIPNESQRTSPSQEQLPLPLNLMSTEDP 694
QY 688 VVACAGHNNQDPSFALLSLNELGERQLVHVWAKALPGFRNLHVDQMAVYQYSWMG 747
Db 695 VIYAGHNTKPTSSLTSLNLQGERQLLSVVKWSKSLPGFRNLHDDQITLLIYQSWMS 754
QY 748 LMVFAMGWSFTNRYMXYAPDLVFNEXYRMHKSWMYSCVVRMHLISQFEGWLTQPOE 807
Db 755 LMVFGLGWSYKHVSQMLYFAPDLILNEQRMKSSYSLCTLMWQIPQEFVKLOVSQEE 814
QY 808 FLCMKALLFSIIPVDGLKNKFFDELRMNYIKELDRILIAKRNKPTSCSRFFVOLTLL 867
Db 815 FLCMKVLLNTIPLGLERSQSFEEMRSSYIRELKAIGLRQKGVVSSSQRYQITKLL 874
QY 868 DSVQPIARELHOFTDILLIKSHMYSVDFFPENMAELISVQVPKILSGVKPIYFH 921
Db 875 DNLHLVQLHLIYCLNTFIQSRLASVFEPPENMSEVIAAQLPKILAGMKPLLFH 928

RESULT 9
ORHP
progesterone receptor form B - human
N:Alternate names: hpr
C:Species: progesterone receptor form A
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1987 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
R:Kastner, P.; Krust, A.; Turcotte, B.; Stropp, U.; Tora, L.; Gronemeyer, H.; Chambon, P.
EMBO J. 9, 1603-1614, 1990
A:Title: Two distinct estrogen-regulated promoters generate transcripts encoding the two
A:Reference number: S09971; MUID:90228361; PMID:2328727
A:Accession: S09971
A:Molecule type: mRNA
A:Residues: 1-933 <KAS>
A:Cross-references: EMBL:X51730
R:Kastner, P.
submitted to the EMBL Data Library, February 1990
A:Reference number: S12464
A:Accession: S12464
A:Molecule type: mRNA
A:Residues: 1-343, 'T', 345-933 <KA2>

A:Cross-references: EMBL:X51730; NID:G35651; PIDN:CAA36018.1; PID:G35652
R:Mirzahi, M.; Alger, M.; D'Aurilio, L.; Loosfelt, H.; Meriel, C.; Fridlansky, F.; Gul
Biochem. Biophys. Res. Commun. 143, 740-748, 1987
A:Title: Complete amino acid sequence of the human progesterone receptor deduced from
A:Reference number: A03245; MUID:87184565; PMID:3551956
A:Accession: A03245
A:Molecule type: mRNA
A:Residues: 1-225, 'G', 227-255, 'V', 257-659, 'V', 661-933 <MIS>
A:Cross-references: GB:M15716; NID:G189934; PIDN:AAA60081.1; PID:G189935
C:Genetics:
A:Gene: GDB:PCR
A:Cross-references: GDB:119493; OMIM:264080
A:Map position: 11q22.1-11q22.3
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: alternative splicing; DNA binding; nucleus; phosphoprotein; steroid hormone
F:1-933/Product: progesterone receptor form B #status predicted <MA>
F:165-933/Product: progesterone receptor form A #status predicted <MA2>
F:565-829/Domain: erba transforming protein homology <ERBA>
F:567-587/Region: zinc finger CCCC motif
F:603-627/Region: zinc finger CCCC motif
F:681-933/Domain: steroid binding #status predicted <STB>
F:41/Binding site: phosphate (Thr) (covalent) #status predicted
F:227,232,552,793/Binding site: phosphate (Ser) (covalent) #status predicted
F:329,374,601/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match

25.7%; Score 1262; DB 1; Length 933;

Best Local Similarity 34.3%; Pred. No. 3.2e-59;

Matches 347; Conservative 123; Mismatches 326; Indels 216; Gaps 33;

QY 38 GPRHPEAASAAP-----PGA-----SLLLLQQQ000000 66
Db 8 GPRAPHVAGGPPSPVSPGLLCPAAGFPFGSQTSLTLPVSAIPISLDGLLFFRPPCQG 67
QY 67 QQQQQQQQQQQQQQETSPRQQQQQGGEDSGPQAHRRGPTGYL--VLDEEQPSPQPSA 124
Db 68 DPSDEKTDQDQSLSDVEGAYRAEATRGAGGSSSPKESGLDSDVLTLLAPSGPGQS 127
QY 125 LECHPERGCVPEPGAAVAASKG--LPQOLPAPPEDESSAAPSTLSLGLTFP-----GL 176
Db 128 -----QSPSPACEVTSSWCLFGPELP-----EDPFAAPATQVLSPLMSRSGCKVGD 174
QY 177 SSCSADLKDIUSE--ASTMOLL-----QQQQQAVS--EGSSSGRAREAG 218
Db 175 SSGTAAAHKVLPRGLSPARQLLPASESPHWSGAPVPSQAAAVEVEEDESSESAG 234
QY 219 APTSSKDNVLTGTSTISDNKELCKAYSVSMGLG-----VEALEHLSPC 262
Db 235 PLLKGPALGGAA--AGGGAACPPGAAAGGVALVPKEDSRFSAPRVALVEQADAPMG 292
QY 263 BOLRG---DCMYAPLLGVPPAVRPTPCAPLAECKGSLDSDAGKSTEDTAESYSPKGY 318
Db 293 RSLATTWDFIHPIL-----PLNHALLAARTQLLEDES-----YDGAGAA 336
QY 319 TKLEGESLGCSS--AAAGSGTLELP-----STLSLY-----KSGALD 356
Db 337 SAFAPRSPSCASSTPVAVGDFPDCAYPDAEPKDDAYPLYDFQPALKIKEEEGA-- 394
QY 357 EAAAYQSRDY-----NFPALAGPPPPPPHARKLENPLDLYGSANAAAA 406
Db 395 EASARSPSYLVAGANPAAPDFPL--GPPPLPP-----RAT 430
QY 407 QCRVGLASLHAGAGAGPGSGPSAAASSWH---TLFTAE-----EGOLYPCGGGGG 458
Db 431 PSRPG-----AAVTAAPASASVSSSSSGSTLECLYKAEGAPPOGFPAPPCAPGA 485
QY 459 GGGGGGGGGGGGGGGGGGAGAVPYGYTRPPQGLAGSDFTPADPVWYGMVSR--VPY 517
Db 486 SGCLLPRDGLPSTASGAAGA--APALY--PALGLNG-----LPOLGYQAAVLKEGLPQ 536
QY 518 PSTCTVKSEMPMMDSYSGPYGDMRLTARDHVLPIDYFP--POKTLICGDEASGCHY 575
Db 537 VYPPYL--NYLRPDSEASQSP-----QYSFESLPKICLICGDEASGCHY 579

Query Match 24.88; Score 1218; DB 2; Length 786;
Best Local Similarity 33.48; Pred. NO. 5.5e-57;
Matches 325; Conservative 128; Mismatches 259; Indels 260; Gaps 30;

progesterone receptor B form - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Aug-1999
 C:Accession: A39596; I49111
 R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.
 Biochemistry 30, 7014-7020, 1991
 A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA encoding the rat mineralocorticoid receptor
 A:Reference number: A39596; MUID:91299759; PMID:2069958
 A:Accession: A39596
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-923 <SCH>
 A:Cross-references: GB:M68915; GB:J05333; NID:g200471; PIDN:AAA39971.1; PID:g200472
 R:Hagihara, K.; Wu-Peng, S.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.
 Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994
 A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the mouse mineralocorticoid receptor gene
 A:Reference number: I49111; MUID:95100931; PMID:7802637
 A:Accession: I49111
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <HAG>
 A:Cross-references: EMBL:U12644; NID:g639916; PIDN:AAA66067.1; PID:g639917
 C:Superfamily: progesterone receptor; erba transforming protein homology
 C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zinc finger
 F:555-819/Domain: erba transforming protein homology <ERBA>
 F:557-577/Region: zinc finger
 F:593-617/Region: zinc finger

Query Match 24.5%; Score 1205; DB 2; Length 923;
 Best Local Similarity 32.2%; Pred. No. 3.2e-56;
 Matches 337; Conservative 119; Mismatches 301; Indels 288; Gaps 36;

QY 35 ONFCPRHPEAASAPP--GASILLQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ-- 86
 DB 7 KDPQVLTGASPSPHIGSPLL-----ARLDGFGQSGHSDYSSVSPISLD 57
 QY 87 -----RQOQQQGGEDGSPQA-----HRRGPTYG-----LVLD 113
 DB 58 GLLFPSCRCRGPDPGKTGQDQSLSDVEGAFSGVEATHREGGRNRPPEKDSRLDSDVLD 117
 QY 114 EQQPSQPSALECHPRGCVPEPFGAASGLPQOLPAPDDEDSAPSTLSLIGTFF 173
 DB 118 SLTPSPGPE---QSHAS---PPACEAITSWCLFGFELP-----EDRSPVPATKGLSP-- 164
 QY 174 PGLSSCSADLKDILSEASTMQLLQOQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ-- 233
 DB 165 -----LMSREIKVGDSQGTGRQ----- 183
 QY 234 ISDNAELCKAVSMGLGVEALEHLSPEQL---RGDCMYAPLLGVPVAVRTPCAPLA 290
 DB 184 -----KVLPGK-----LSPPRQLLPTSGSAHWPAGVKPS---PQPA-- 219
 QY 291 ECKGSLDSDSAGKSTEDTAESYPPKGYTKGLEGESIG---CSGSAAGSSGTLEPSTL 347
 DB 220 ---GEVEDS---GLTEGSA---SPLKSKPRALGEGTGGGGVAANAFSAAPGGVTLVPKED 273
 QY 348 SLYKSGALD-----EAAAYQSRDYNFPL-----A 372
 DB 274 SRFSAVPSLEQDSPIAPGRSPLATTVDFTHVPLPILNHALLAARTROLLEGESYDGA 333
 QY 373 LAGPPPPPPPP-----HPHARKLEN-----PLDYGSAWAAAAAOCRYGDLA 414
 DB 334 TAGPFCPPRSPASPTVPVRGDFPDCTYPLEGDKEDYFPL-----YGDQ 379
 QY 415 S-----LHGAGAAGPGSGSP-----SAAASSWHLTFTAEQQLYGPCCGGGGGGGG 462
 DB 380 TPLGLKKEEEGADAA---VRSRPLYSAGASSSTFPDFPLAPAPQAAPASRRPGEAAVAG 436
 QY 463 GGGGGGGGGGGGGA-----CAVAPYGYTRP-----QGLAQESD 499
 DB 437 GPSSAAVSPASSSGSALFECILYKAEAPPTQGSFALP--CKPPAAASCLLPRDSLPAAPT 495
 QY 500 FTAPDWPVPGGMVSRVPSPSTCVKSEMPWMDSYSGPYGDMRLLETARDHVLPP--IDYF 557
 DB 557 ----- 557

DB 496 AAPATYQPLGL--NGLP-----QLG-----YQAAVLKDSLPQVVPVPPVLYLNR 536
 QY 558 P-----PQKTLICGDEASCHYALTGCGSKCVFFKRAAEGKQKYLCA 602
 DB 537 PDSEASQSPQGFDSLQKICLICGDEASCHYGVLTGCGSKCVFFKRAEGQHNYLCAGR 596
 QY 603 NDCTIDFRNRKNCPSCLRYEAGMTLGARKLKKLNKLQE--EGEA--STTTSPT 658
 DB 597 NDCIVDKIRRNKNCPCARLKKCCQAGVGLGKFKKFKKVRMRTLDGVALPQSVGLPNES 556
 QY 659 --TTOKLTSHIEGECOPFLNLEAIEPCVVCAGHNNQPDPSFAALLSSLNELGERQL 716
 DB 657 QALSORITFSNQEIQLVPPPINLMSIEPDVYVAGHNTKPDTSSTSLTSLNOLGERQL 716
 QY 717 VHVVKAKALPFRNLHVDVDDOMAVIQYSWGLMVFANGWRSFTNVSNMRYLPADLVFNE 776
 DB 717 LSVVKKSKSLPFRNLHVDVDDOMAVIQYSWGLMVFANGWRSFTNVSNMRYLPADLVFNE 776
 QY 777 YRMHKSRYMSQCVRMHLSQEFQWLOITPQEFCLMKALLFIIPVDGLKNQKFFDELRM 836
 DB 777 QRMKELSYSLCTMMQIPQEFVKLVQVTHEEFLCMKVVLLNTLPIELRSQSOFEMRS 836
 QY 837 NYIKELDRITIAKRNKPTSCSRFFYQLTKLDSVQPIARELHQFTDLLIKSHMVSVDFP 896
 DB 837 STIRELIKAIGLRQKGVVPTSORFYQLTKLDSLHDLVKQLHLYCLNTFIQSRTIAVEFP 896
 QY 897 EMMAELISVQVVKILSGKVKPIYFH 921
 DB 897 EMMSEVIAAQLPKILAGMVKPLLFH 921

RESULT 13
 A41401
 mineralocorticoid receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 20-Sep-1999
 C:Accession: A41401
 R:Fater, P.D.; Sherman, T.G.; Goldman, D.J.; Watson, S.J.
 Mol. Endocrinol. 3, 1877-1885, 1989
 A:Title: Molecular cloning of a mineralocorticoid (type I) receptor complementary DNA
 A:Reference number: A41401; MUID:90114194; PMID:2558305
 A:Accession: A41401
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-981 <PAT>
 A:Cross-references: GB:M36074; NID:g205340; PIDN:AAA41583.1; PID:g205341
 C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
 C:Keywords: DNA binding; transcription regulation; zinc finger
 F:602-877/Domain: erba transforming protein homology <ERBA>
 F:604-624/Region: zinc finger
 F:640-664/Region: zinc finger

Query Match 22.2%; Score 1092; DB 2; Length 981;
 Best Local Similarity 32.0%; Pred. No. 3.2e-50;
 Matches 310; Conservative 119; Mismatches 306; Indels 234; Gaps 34;

QY 77 QOQOQOQTSPPR---QOQOQOQEDGSPQAHRRGPTGYLVLDDEQOQSPQOSA----- 124
 DB 121 QOQOQOQSLPTKIYQNMQLVKYKENGHRSTLS--AMSRPLRSFMPDAAAMNGALR 178
 QY 125 -----LECHPERGCVPEP---GAANAASKGL-----PQQLPAPDEDDSA 162
 DB 179 AIVKSPIIICHKEKSSVSSPLNMASSVCSVPGINSMSSTTSFGSPVHSPHTQGTSLICS 238
 QY 163 PST-----LSLLGPTFFGLSSCSADLKDILSEASTMOLLOQ 198
 DB 239 PSVNRGRSRSHPSHASVNSVPSLSSPMKSPISPPSHCS--VKSPSSPNVPLR 296
 QY 199 QOQEA-----YSEGSSGRAREASGAPTSSKDNVLGTSTISDNKELKAVSVNG 250
 DB 297 VSSPANLNNSRCSVSSPNNNTNRTSLTSSPTASTVSGIG--SPISNAFVATSGAGAGAG 354
 QY 251 LGVEALEHLSFG---EQLRGDCMYAPLLGVPVAVRTPCAPL-----AECGSLDD 299

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Db 355 ---AIDVSPDTHKGAHVPFKTEVERKAISNGVTGPNLNIYQYIKSPDGAFASS 410
QY 300 SAGSTEDTARYSPFKGYTKGLESLGCGSAAAGSGTLELPSTLSLYKSGALDEAA 359
Db 411 CLGNSK-ISPSSPFSVPIKQ--ESSKHSCGSGAFSGNFTVNPFPMDGSGYFS-FWDD-- 464
QY 360 AYQSRDYNFLALAGPPPP-----PPPHPHARIKLENPLDYGSAMAAAAQCRYGDL 413
Db 465 ----KDYISLS-GILGPPVPFGDSCDSAFP--VGIKQEPDGS-----YYPE 506
QY 414 ASLHGACAGCGSGSAAASSWHILFTAEGLYKPGCGGGGGGGGGGGGGGGGGGG 473
Db 507 ASIPSSAIVGNSG-----GQSFHY----- 526
QY 474 GGGEAGAVAPYGYTRPPQGLAGSDFTAPDVWYPGMVSRVPYSPPTCVKSEMGPWMS 533
Db 527 ---RIGAQTISLSRSPDQSFQH-----LSSFP-PVNTLVES-----WK-- 562
QY 534 YSGPYGDMRLTARDHVLIDYFP-----PQKTLICGDEASGCHYG 576
Db 563 ---PHGD--LSSRRSDGYPVLEYIPENVSSTLRSYSTGSSRPSKICLVCGDEASGCHYG 617
QY 577 ALTCGCKVFKKRAAGKQKYLCAASNDCTIDKFRKNCPCSLRKYAEAGMTLGARKLK 636
Db 618 VFTGCKVFYKRAVEGQHNLYLCAGNRDCTIDKIRKNCPCACRLQKCLQAGMNLGARKSK 677
QY 637 KLNK-LQEE-----GEASSTTSPTTEET-----QKLTVSHIEGYEQP 675
Db 678 KLKGLKGLHEEQPQPPPPPPQSPPEGTTYIAPTKEPSVNSALVQLTSTITH-----ALTP 733
QY 676 IFNLVLEATEPGVVCAGHNNQPDFAALLSLNELGERQLVHVYKAKALPGRNLHVD 735
Db 734 SPAMILENLEPETVYAGDINSKPDFAESLLSTLNRLAAKQMIQVVKAKVLPFGKPLPE 793
QY 736 DQNAVTOYSWMGLVFAMGWSFTNVNSRMILYFAPDLVFNRYMHKSMYSCQVRMHL 795
Db 794 DQITLIQYSWMLSSFALSWSRSYKHTNSQLLYFAPDLVFNRYMHKSMYSCQVRMHL 853
QY 796 QEFGLQITPOFLCKWALLLSIIPVGLKNQKFFDELNMNYIKELDRIIACKRNKPTS 855
Db 854 LOFVRLQITFEYSIMKVILLLSLTPKDKLQSAFAEEMRTNYIKELRKMT---KCPNS 910
QY 856 CS---RRFYQLTKLSDVQIARELHOFTFOLLKSHMVSVDPEMMAELISVQVPKLS 912
Db 911 SGQSWQRYQLTKLSDHVLSDLEFCFTFFRESQALKEVFPFAMLVLEIITDOLPKVES 970
QY 913 GKVKPIYFH 921
Db 971 GNAKPLIYFH 979

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RESULT 14
A29513
Mineralocorticoid receptor - human
N:Alternate names: aldosterone receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Sep-1999
C:Accession: A29513
R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, T.M.; Handelin, B.L.; Housman, D.E.
Science 237, 268-275, 1987
A:Title: Cloning of human mineralocorticoid receptor complementary DNA: structural and
A:Reference number: A29513; MUID:87263386; PMID:3037703
A:Accession: A29513
A:Molecule type: mRNA
A:Residues: 1-984 <ARR>
A:Cross-references: GB:M16801; NID:g187460; PIDN:AAA59571.1; PID:g307166
C:Genetics:
A:Gene: GDB:MLR
A:Cross-references: GDB:120186; OMIM:264350
A:Map position: 4q31-4q31
C:Superfamily: unassigned erba-related proteins; erba transforming protein homology
C:Keywords: DNA binding; transcription regulation; zinc finger

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F:601-880/Domain: erba transforming protein homology <ERBA>
F:603-623/Region: zinc finger
F:639-663/Region: zinc finger

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Query Match 22.0%; Score 1078.5; DB 2; Length 984;
Best Local Similarity 32.8%; Pred. No. 1.6e-49;
Matches 300; Conservative 101; Mismatches 254; Indels 259; Gaps 30;

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QY 98 SPQARRRGPTGYL-----VLDEEQP-SQPOSALCEHPERCVPPEP--GAVAASK 145
Db 238 SPANRGRSHSHPAHASNVGSPLSPLSSMKSSISSPPSHCSVKSVPSSNNVTLRSSV 297
QY 146 GLPQQL-----PAPDEDD-----SAAPSTL-SLLGP-----TFPGLSSCADLKD 185
Db 298 SSPANTNNRCVSSPSNTNRSSTLSSPAASTVGSICTSPVNNAFSYTASCTAGSSTLSD 357
QY 186 ILSEASTMOLLOQ-----OEAIVSEGSSSGRA-----REASGAPT-SKKNYLGCT 231
Db 358 VVPSPTQKGAQVFPFKTEEVESAINGVTCQNLIVQYIKPEPDGAFSSS---CLGNN 414
QY 232 STISDNAKELCAVSVSMGLVGEALHLSPEQLRGDCMYAPLLGVPPAVPRTPCAPLAE 291
Db 415 SKINDS-----SFSVPKQESTKHSCSGTSFKGN-----PTVNPFP-----451
QY 292 CKGSLDDDSAGKSTEDTAEY--SPFKGGYTKLEGESLGCSSGAAGSSGTLELPSTLSL 349
Db 452 ----FMDGSYFMDKDYISLGLGPPVPFGD-----NCEGS-----487
QY 350 YKSGALDEAAAYQSRDYNYFNPLALAGPPPPPPPHPHARIKLENPLDYGSAMAAAAQCR 409
Db 488 -----GFPVGIKQEP-----DDGS-----501
QY 410 YGDLASLHCAGNAGCGSSPSAAASSSWHTLFTAEGLYKPGCGGGGGGGGGGGGGG 469
Db 502 YYPEASIPSSAIVGNSG-----GQSFHY-----525
QY 470 GGGGGGGEAGAVAPYGYTRPPQGLAGSDFTAPDVWYPGMVSRVPYSPPTCVKSEMGP 529
Db 526 -----RIGAQTISLSRSARDOSFQH-----LSSFP-PVNTLVES-----559
QY 530 WMSYSGPYGDMRLTARDHVLIDYFP-----PQKTLICGDEASG 572
Db 560 WKS-----HGD--LSSRRSDGYPVLEYIPENVSSTLRSYSTGSSRPSKICLVCGDEASG 612
QY 573 CHYGALTCGCKVFKKRAAGKQKYLCAASNDCTIDKFRKNCPCSLRKYAEAGMTLGA 632
Db 613 CHYGVVTCGCKVFYKRAVEGQHNLYLCAGNRDCTIDKIRKNCPCACRLQKCLQAGMNLGA 672
QY 633 RKLKLNK-LQEEGEASS-----TTSPTTEET-----QKLTVSH 667
Db 673 RSKKLGKLGHEEQPQPPPPPPQSPPEGTTYIAPAKEPSVNTALVQLSTISR 732
QY 668 IEGYECOPIFNLVLEATEPGVVCAGHNNQPDFAALLSLNELGERQLVHVYKAKALP 727
Db 733 ----ALTPSPVWLENLEPELVYAGDINSKPDFAESLLSTLNRLAGKQMTQVVKAKVLP 788
QY 728 GFRNLHVDQMAVIOYSWMGLVFAMGWSFTNVNSRMILYFAPDLVFNRYMHKSMYSCQ 787
Db 789 GFKNLPLEDQITLIQYSWMLSSFALSWSRSYKHTNSQLLYFAPDLVFNRYMHKSMYSCQ 848
QY 788 CVMRHLSEQFWLOITPOFLCKWALLLSIIPVGLKNQKFFDELNMNYIKELDRITA 847
Db 849 CQGMHQISLOFVRLQITFEYSIMKVILLLSLTPKDKLQSAFAEEMRTNYIKELRKMT 908
QY 848 CKRNKPTSCRRFYQLTKLSDVQIARELHOFTFOLLKSHMVSVDPEMMAELISVQV 907
Db 909 KCPNNSQSWQRYQLTKLSDHVLSDLEFCFTFFRESQALKEVFPFAMLVLEIISDOL 968
QY 908 PKLSGKVKPIYFH 921
Db 969 PKVESGNAKPLIYFH 982

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Query Match	21.7%	Score	1065;	DB	1;	Length	795;
Best Local Similarity	32.0%;	Pred.	No. 6.7e-49;				
Matches	314;	Conservative	110;	Mismatches	288;	Indels	288;
Gaps							35;
Qy	20	GAFAONLFQSVR---	EVTONPGRHPEAASAPPGASLILL-----	QQQQQQQQQQQQ	68		
		: : : :	: : :				
Dd	24	RGSVMDFFYKSLRGATVKVSASSVAANQADSKQRILLDFSGKSTSNVQROOQQQQ	83				
Qy	69	QQQQQQQQQQQQQQQTSP-----	RRQQQQQGED-GSQPAHR----	RGPTGGLVL	112		
		:	: : : :				
Dd	84	QQQQQQQQQQQQQGLSKAVSLMSGLMYGETETKYMGNDLGYPPQQQLGSSGETFRLL	143				
Qy	113	DE----EQPSQPOSALECHPERGVCPBPGEAAVAASKGLPOOLPAPPDDEDSDAAPSTLS	167				
		: : : : : :	:				
Dd	144	EESIANLNKSTSVENPKSSTSATGC-----	ATPEKE-----	176			
Qy	168	LIGPTFPGLSCSADLKDLTLPASTWMLLQQQQQEAIVSEGSSGSRAREASGAPTSEKDNY	227				
		: : : : :	: : : : :				
Dd	177	----FKPTH-----SDASS-----EQNKRKSQTGTNGG-----	SVKLY	205			